FIG. 1A

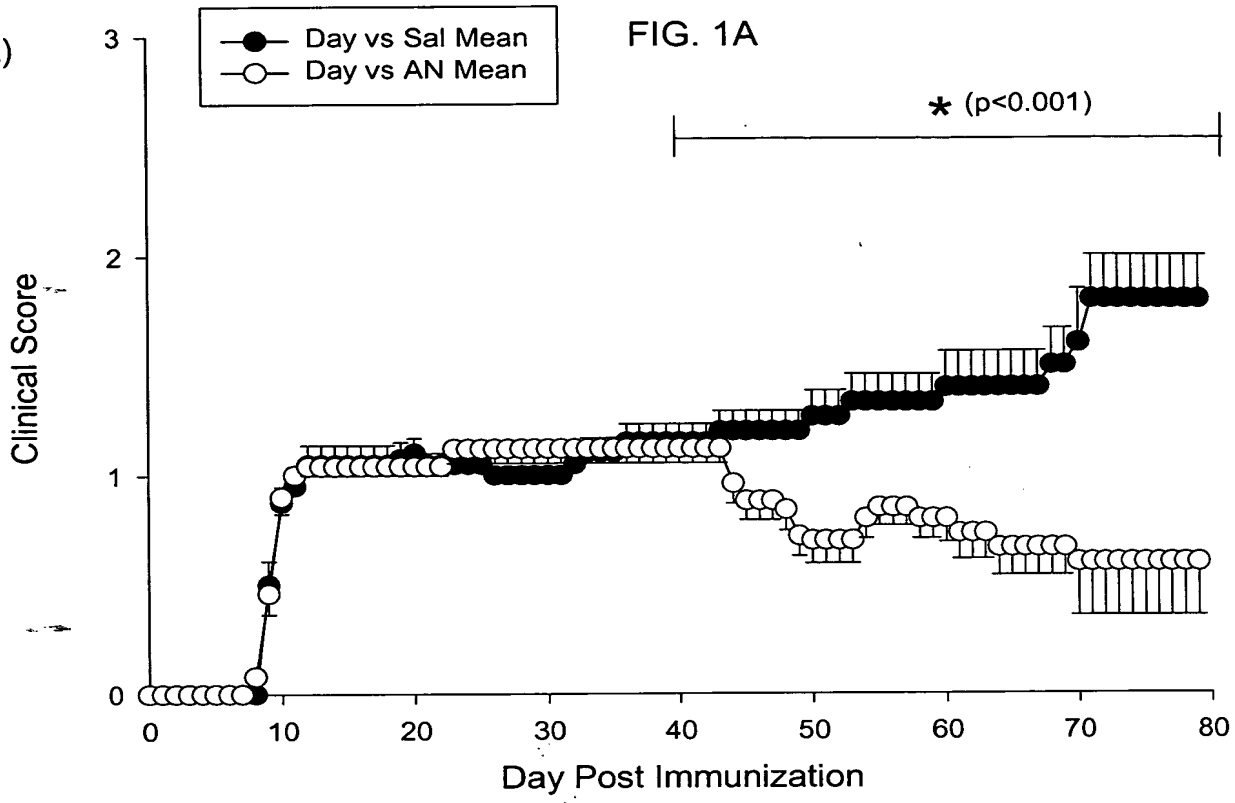
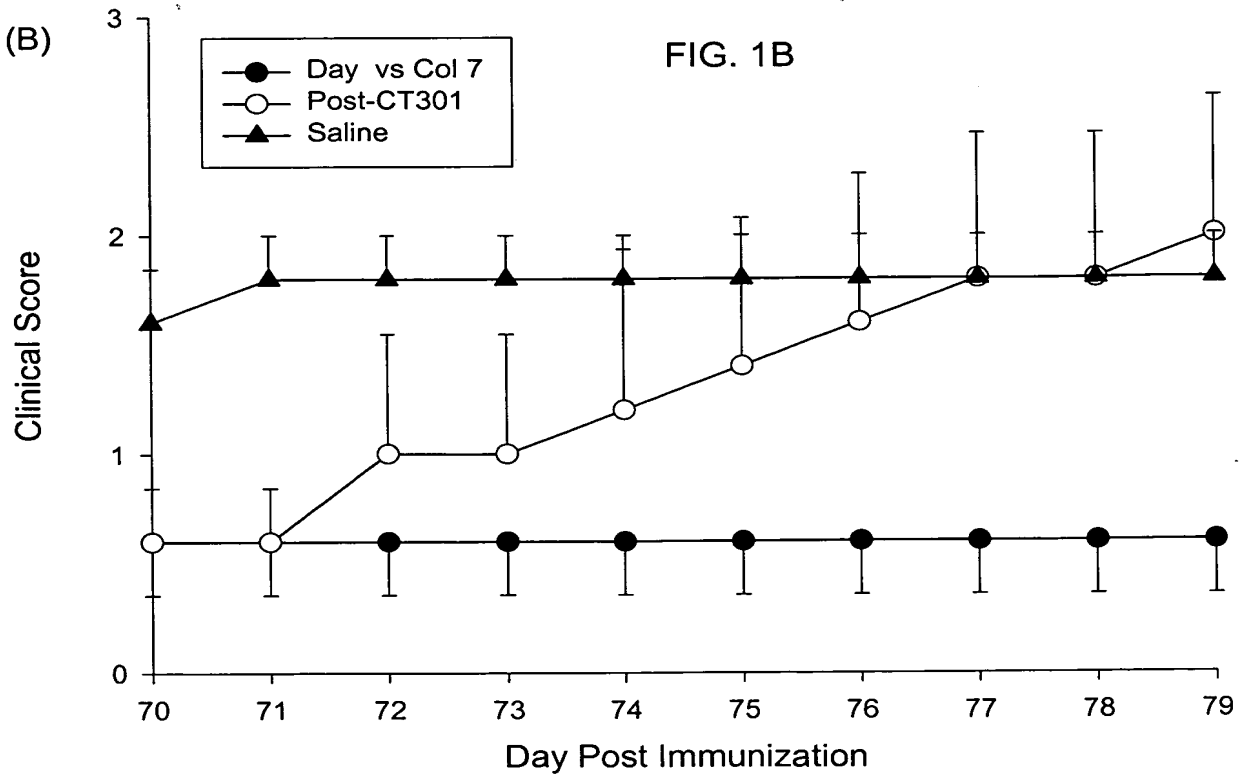


FIG. 1B



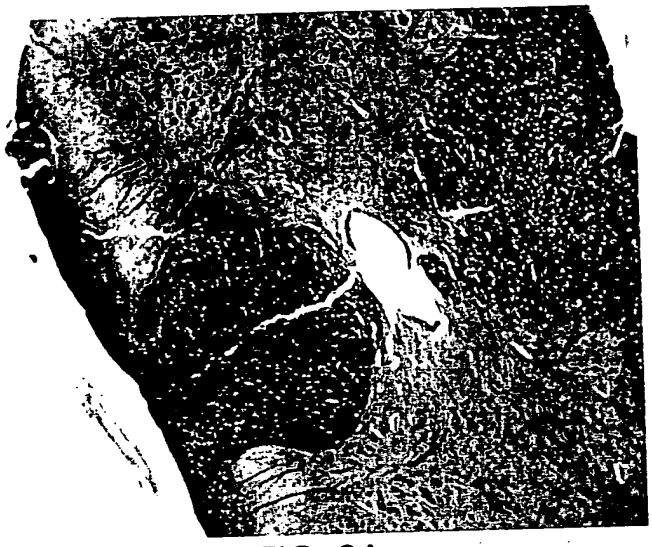


FIG. 2A

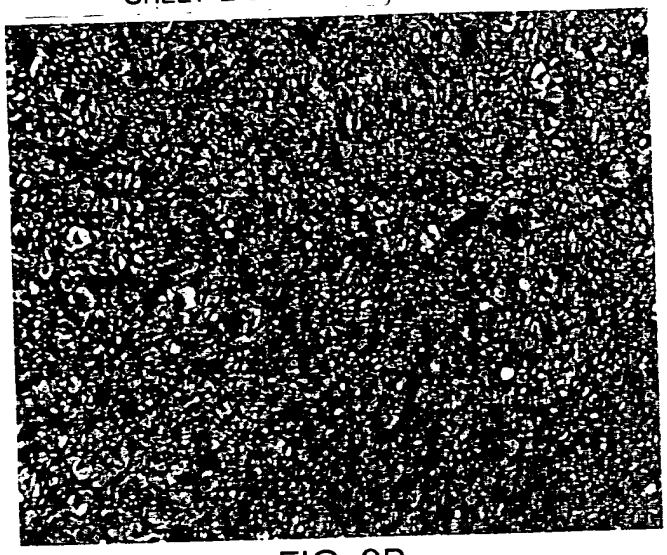


FIG. 2B

FIG. 2C

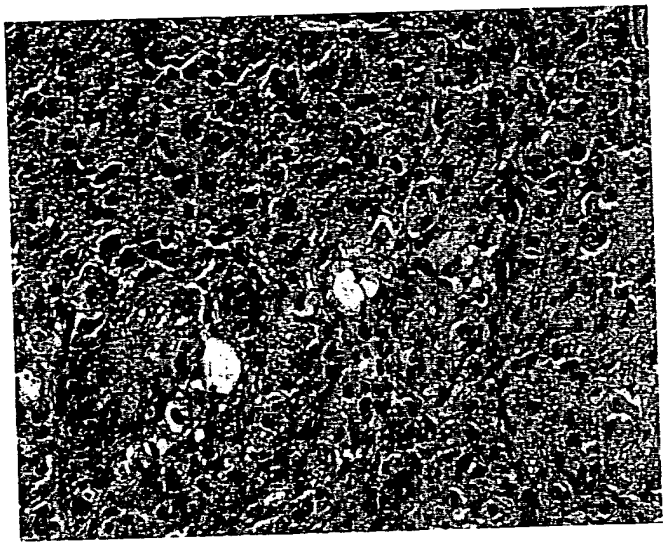


FIG. 2D

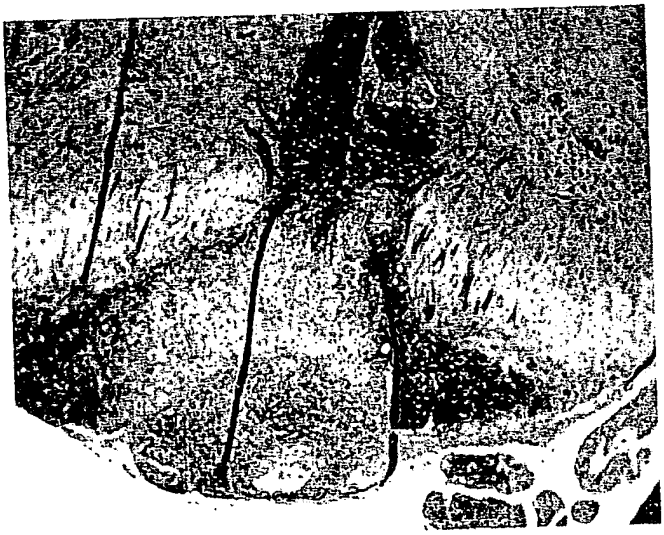


FIG. 2E

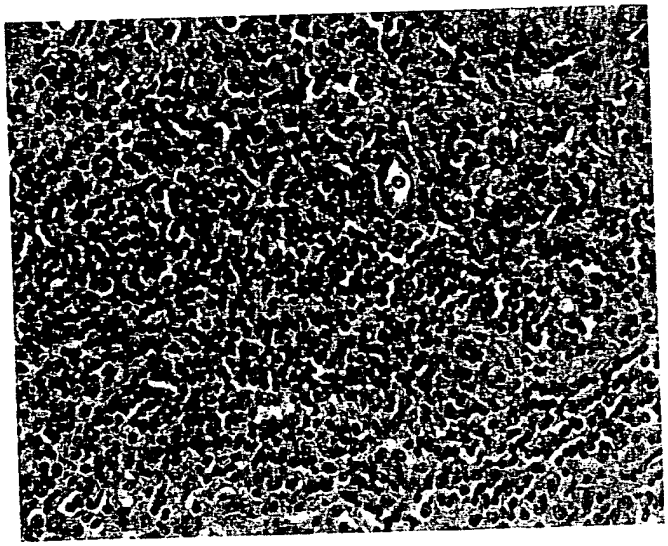


FIG. 2F

FIG. 2G

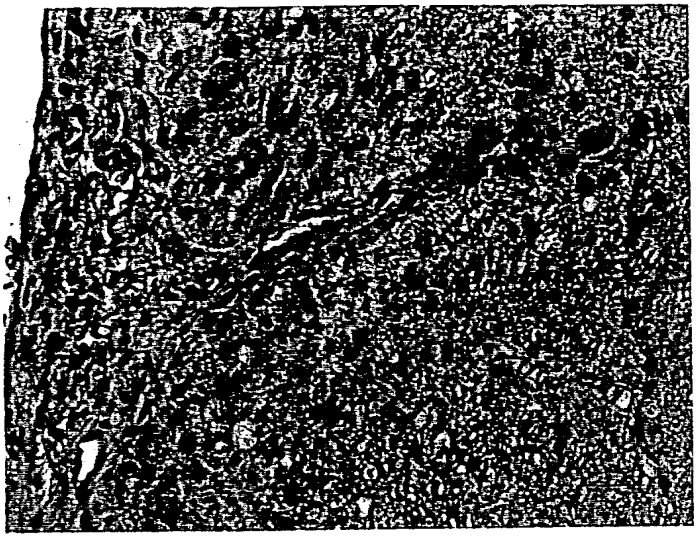


FIG. 2H

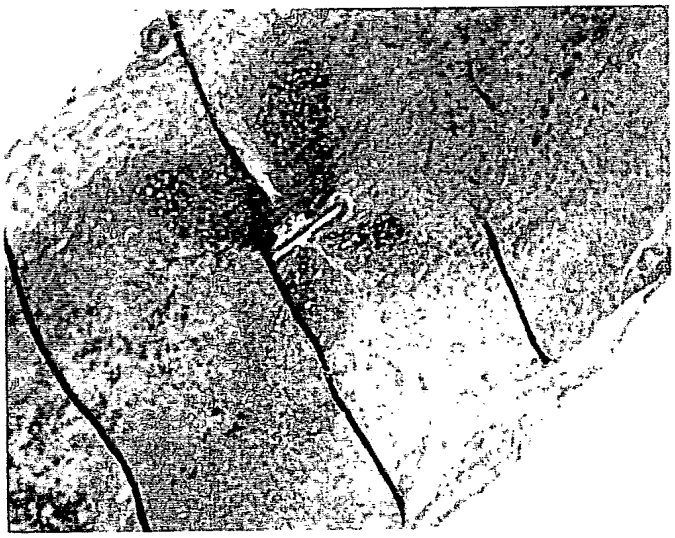


FIG. 2I

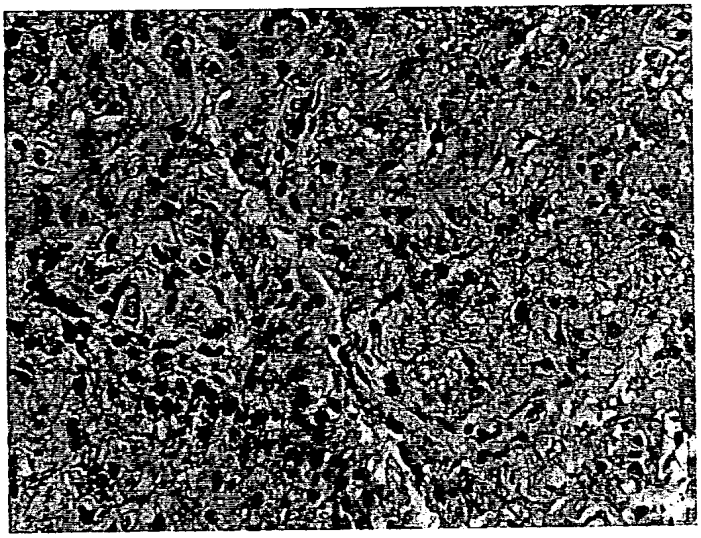


FIG. 2J

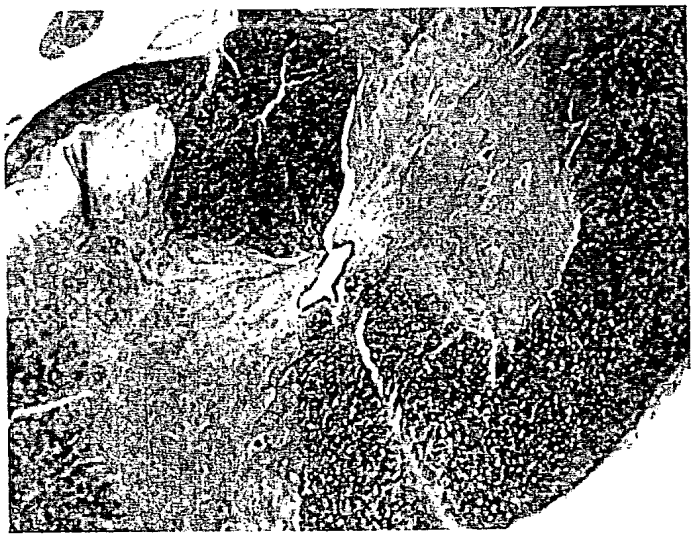


FIG. 2K

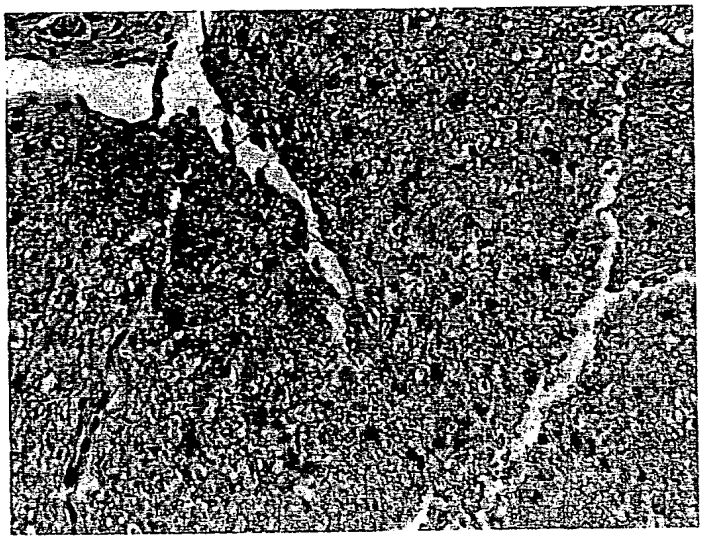


FIG. 2L

FIG. 3A

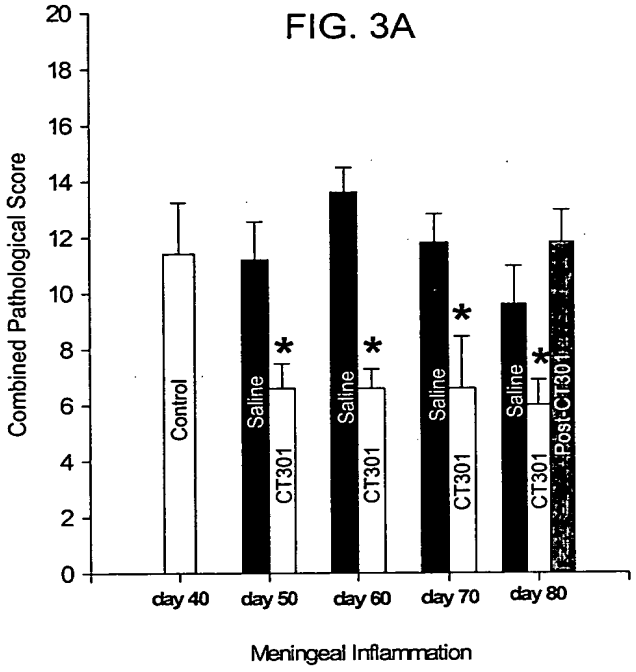


FIG. 3B

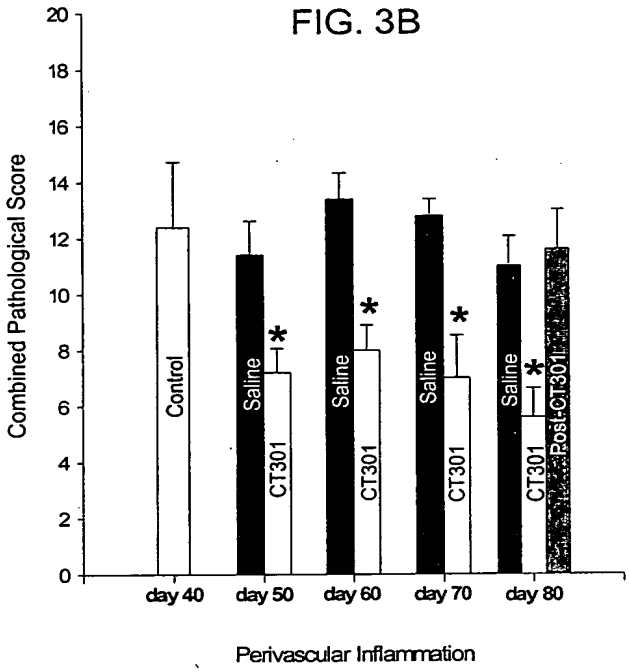


FIG. 3C

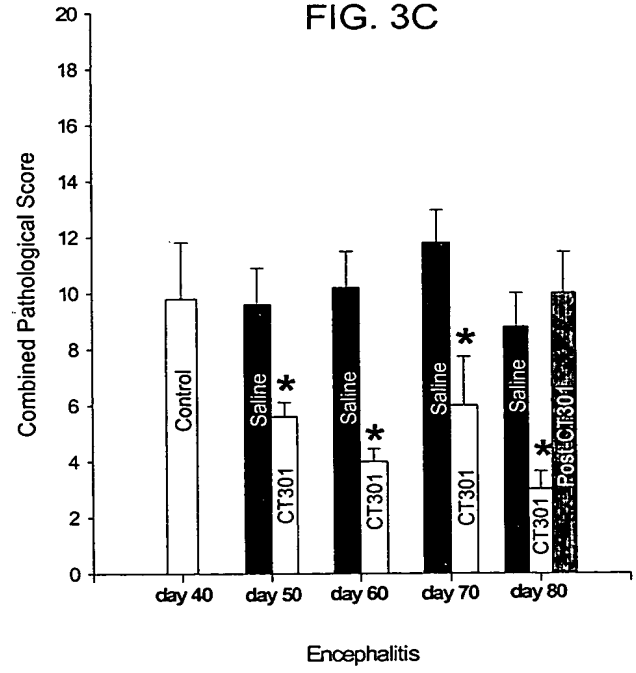
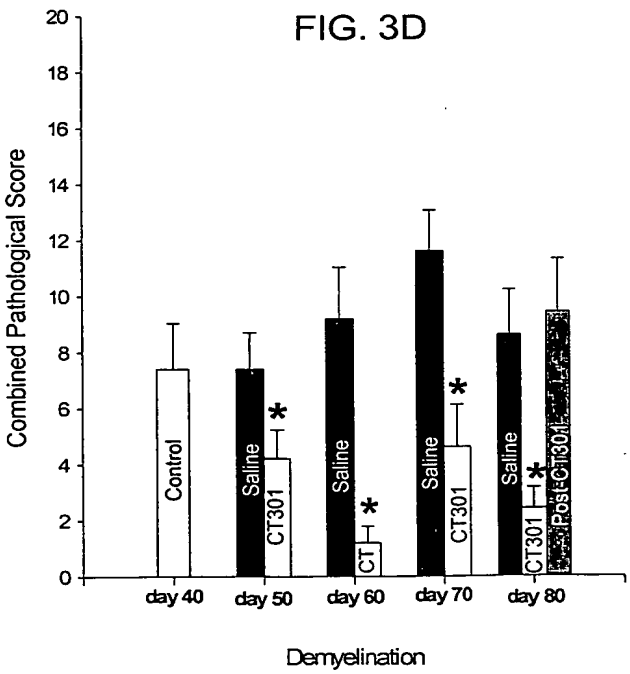


FIG. 3D



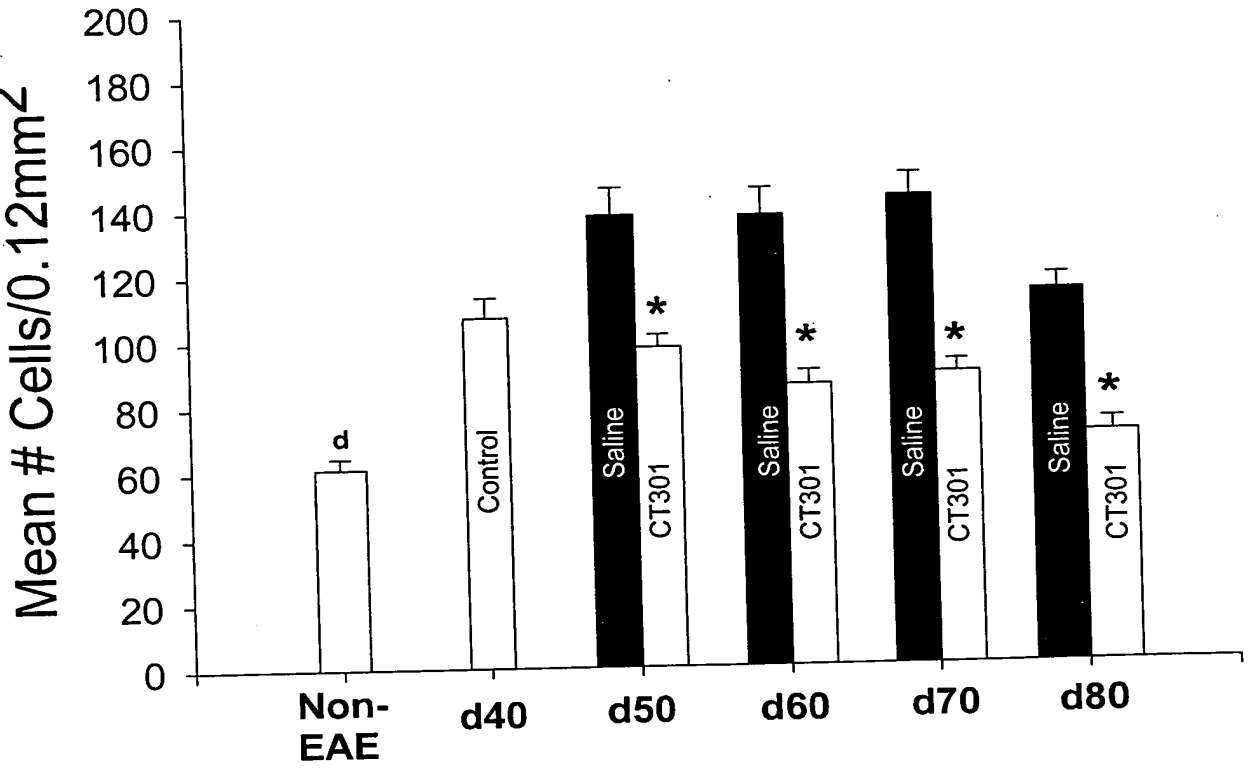
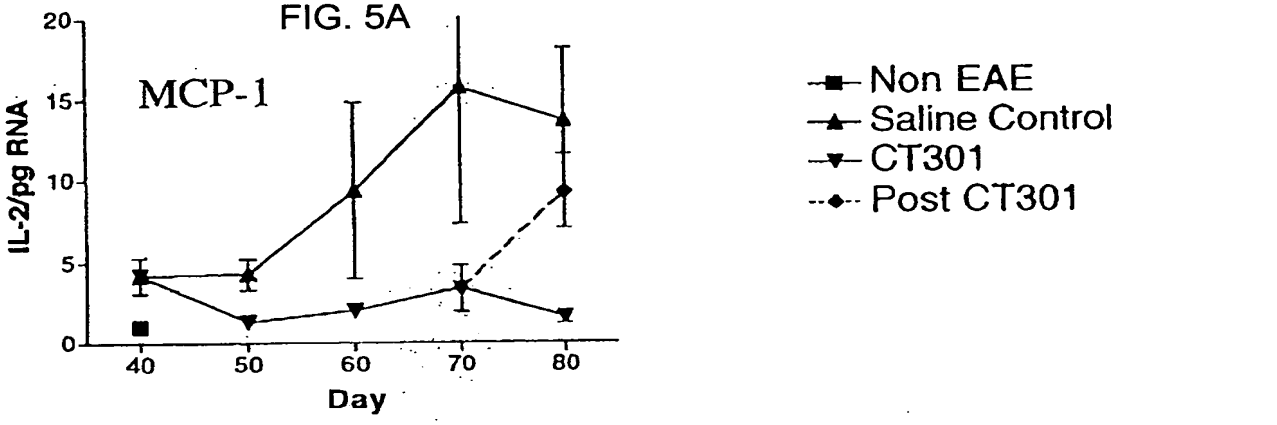
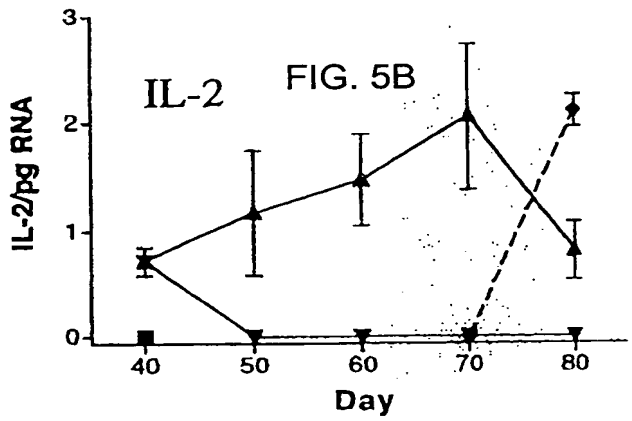
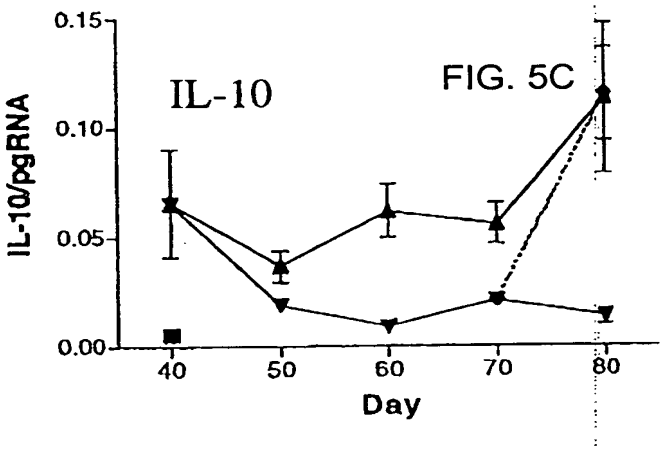

Mean # Cells/0.12mm2
200
180
160
140
120
100
80
60
40
20
0
d
Control
Saline
CT301
Saline
CT301
Saline
CT301
Saline
CT301
*
*
*
*
Non-EAE
d40
d50
d60
d70
d80

FIG. 4

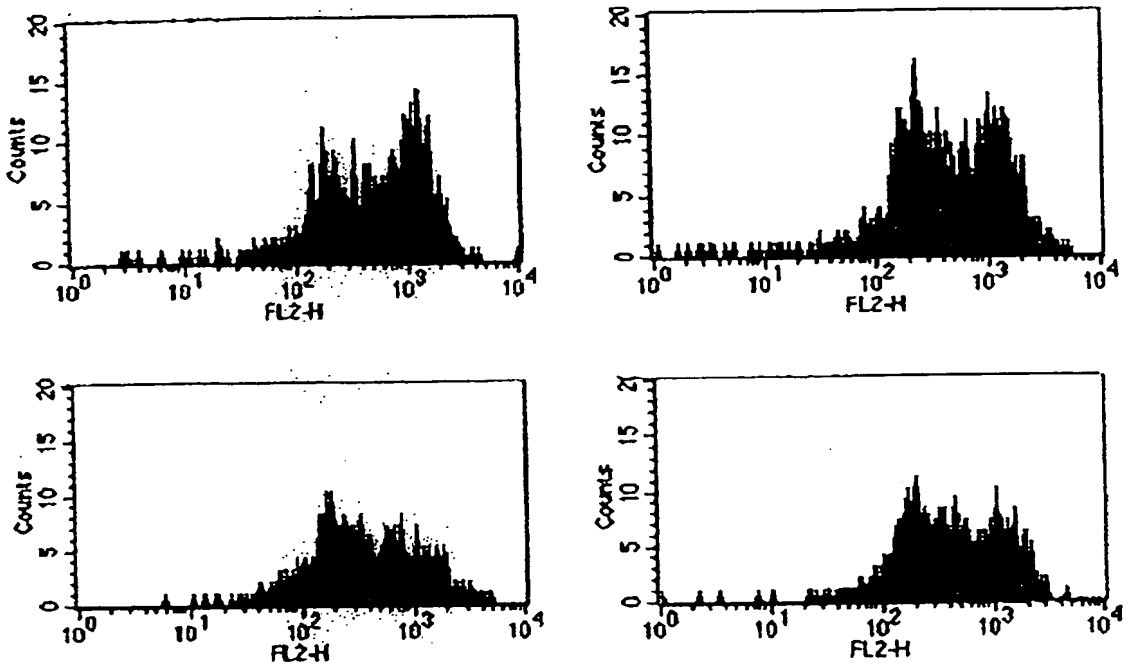
FIG. 5A


MCP-1
IL-2/pg RNA
20
15
10
5
0
40
50
60
70
80
Day
Non EAE
Saline Control
CT301
Post CT301


IL-2
FIG. 5B
IL-2/pg RNA
3
2
1
0
40
50
60
70
80
Day


IL-10
FIG. 5C
IL-10/pgRNA
0.15
0.10
0.05
0.00
40
50
60
70
80
Day

CT301



Saline

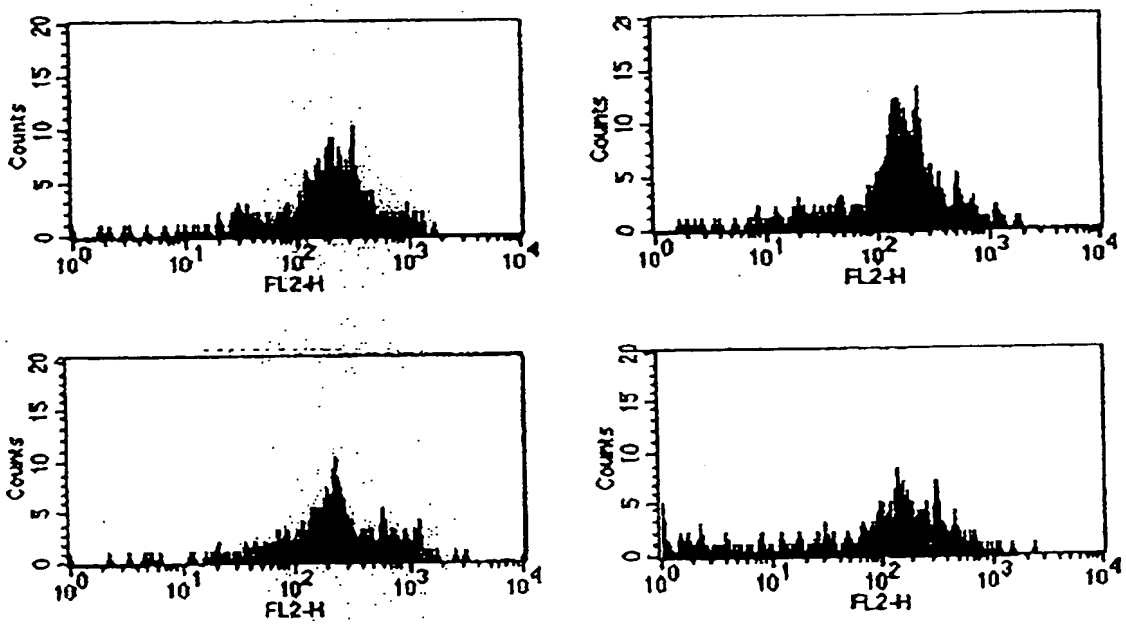


FIG. 6

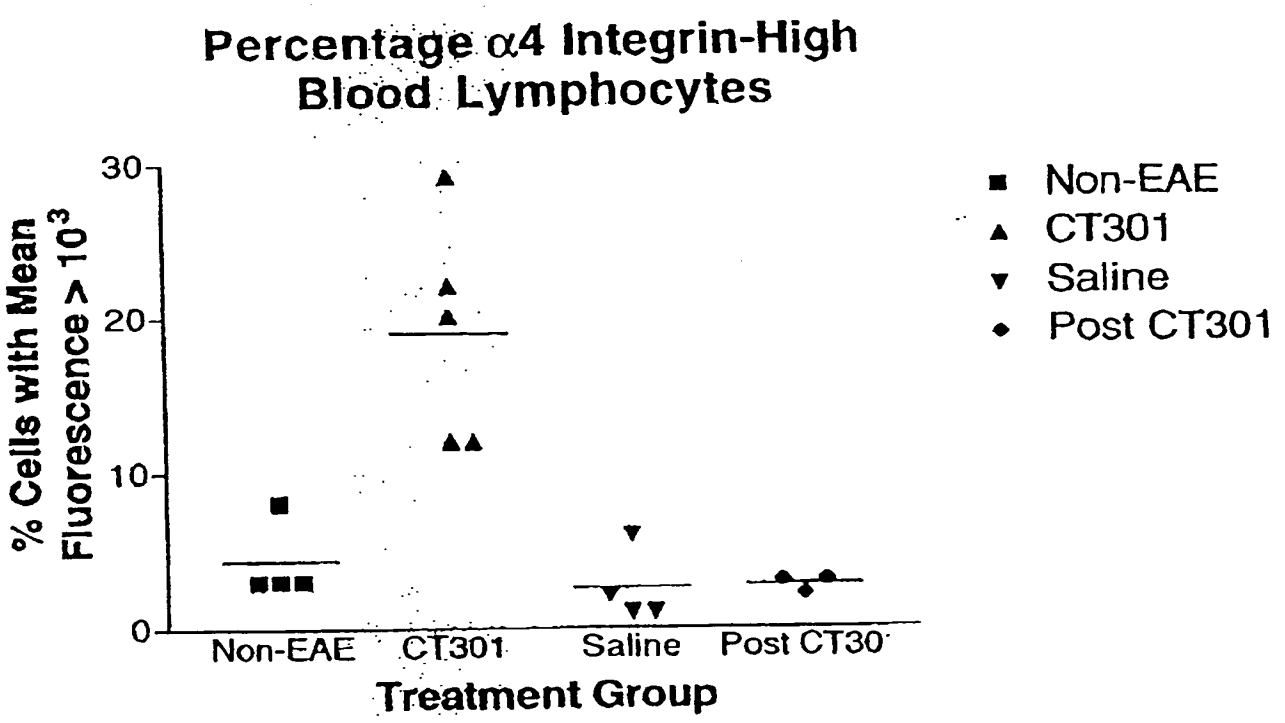

Percentage α4 Integrin-High Blood Lymphocytes
% Cells with Mean Fluorescence > 10^3
30
20
10
0
Non-EAE
CT301
Saline
Post CT30
Treatment Group
Non-EAE
CT301
Saline
Post CT301

FIG. 7A

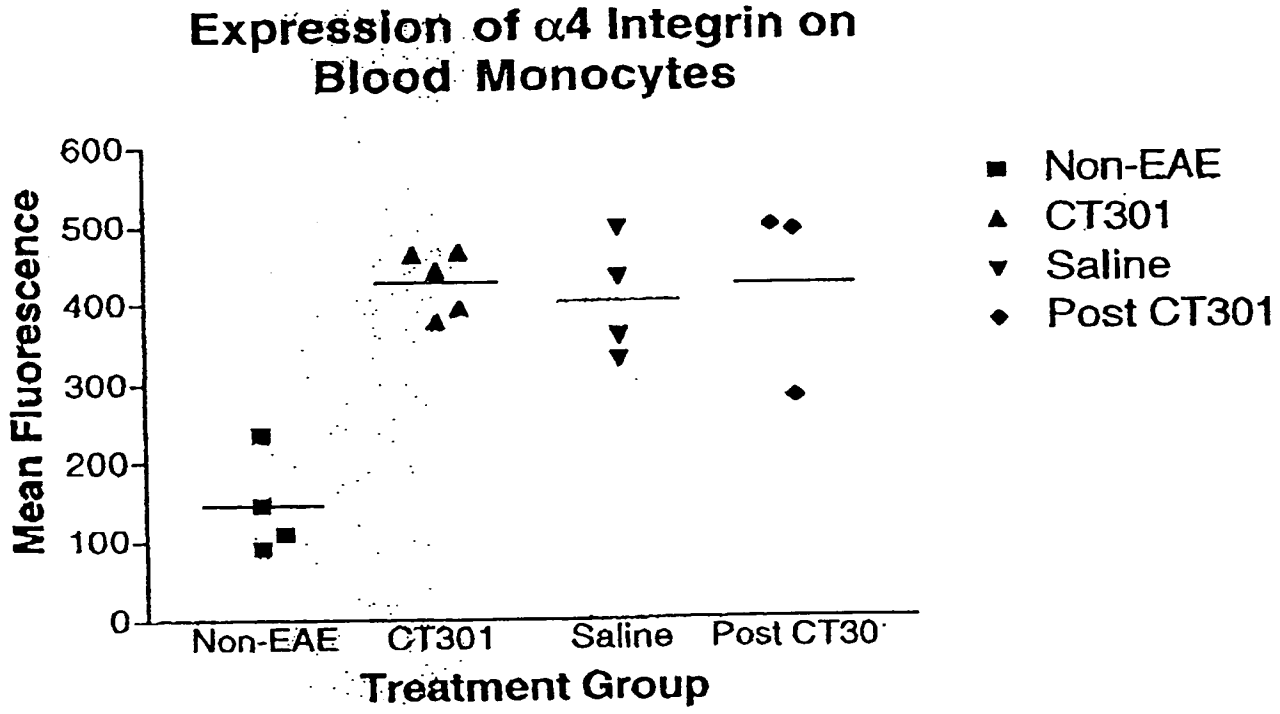

Expression of α4 Integrin on Blood Monocytes
Mean Fluorescence
600
500
400
300
200
100
0
Non-EAE
CT301
Saline
Post CT30
Treatment Group
Non-EAE
CT301
Saline
Post CT301

FIG. 7B

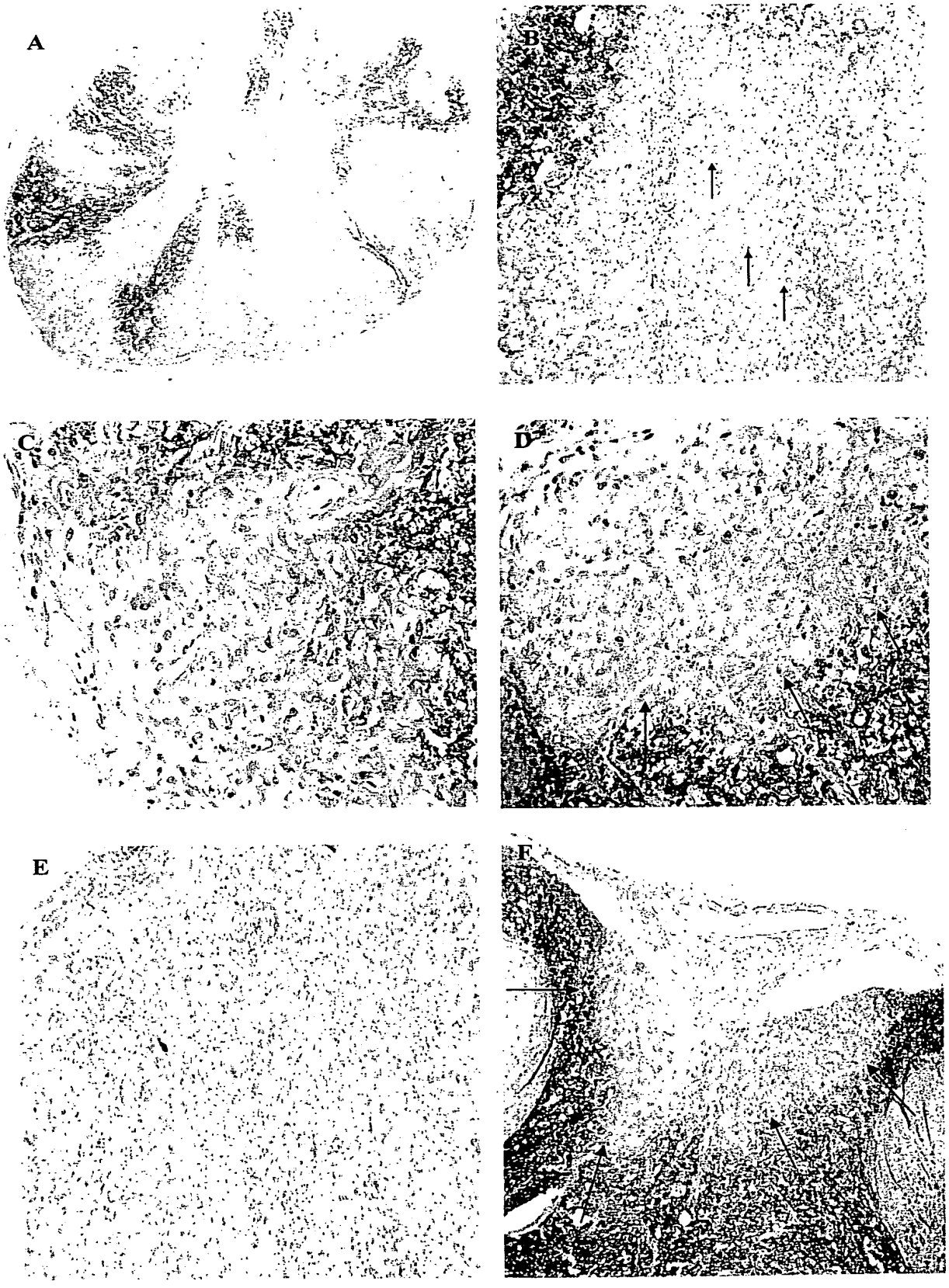


FIG. 8

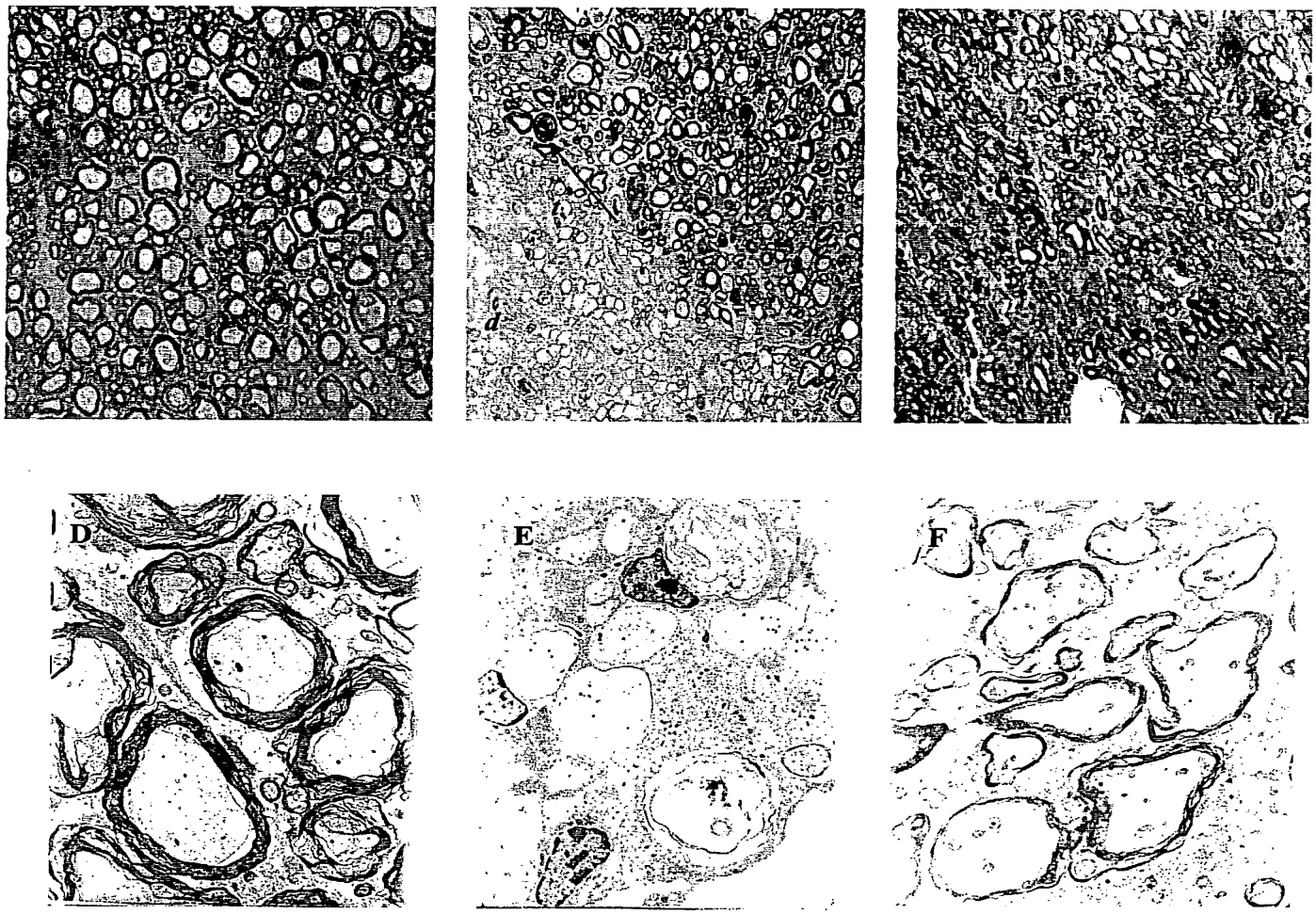


FIG. 9

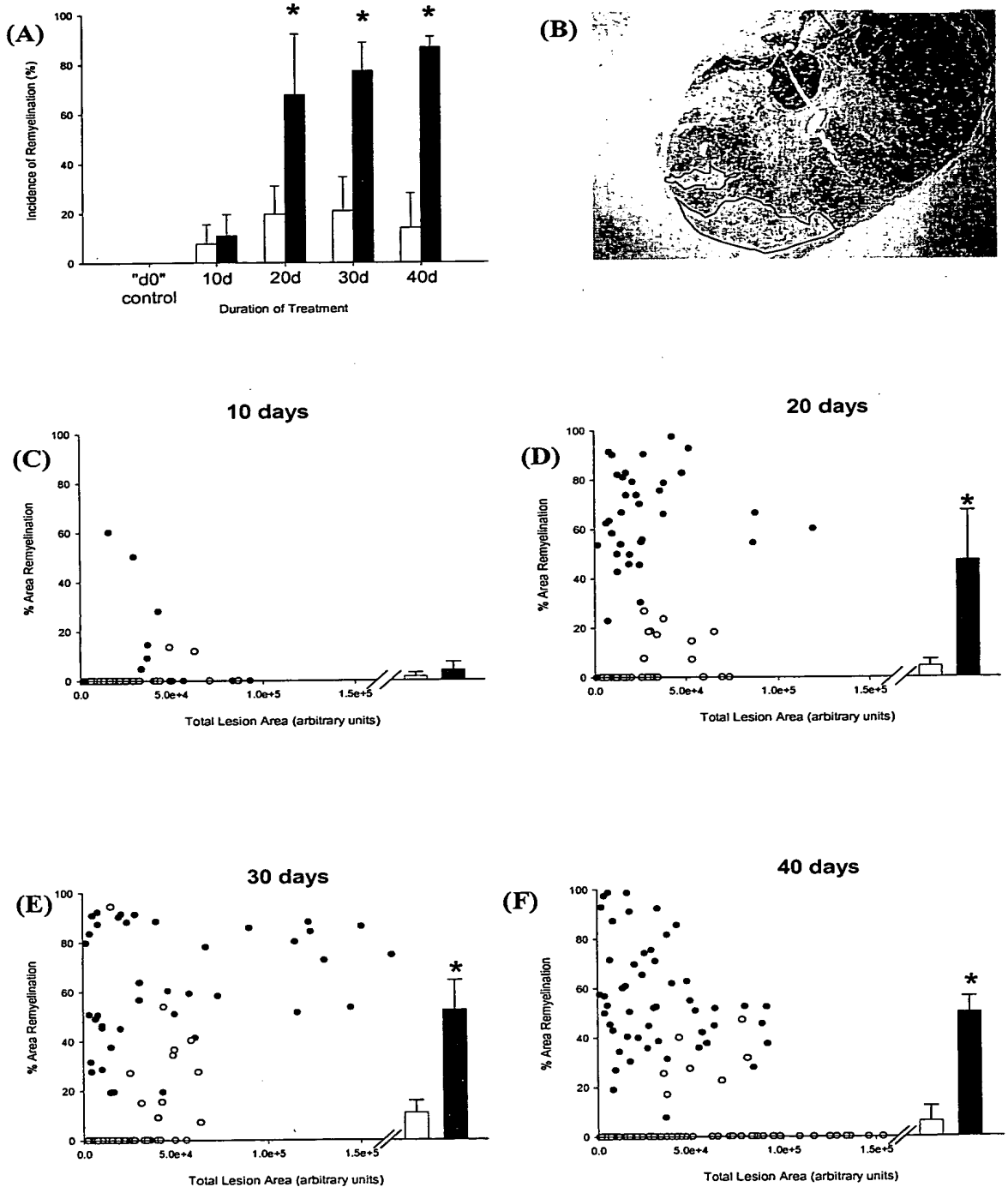

(A)
Incidence of Remyelination (%)
"d0" control
10d
20d
30d
40d
Duration of Treatment
(B)
10 days
(C)
% Area Remyelination
Total Lesion Area (arbitrary units)
20 days
(D)
% Area Remyelination
Total Lesion Area (arbitrary units)
30 days
(E)
% Area Remyelination
Total Lesion Area (arbitrary units)
40 days
(F)
% Area Remyelination
Total Lesion Area (arbitrary units)

FIG. 10

```
      atgagggcccctgctcagatttttggattcttggtcaggagacgttgt
    1 ----------------------------------------------------
      tactcccggggacgagtctaaaaacctaagaaccagtcctctgcaaca

      agaaatgagaccgtctattcagttcctggggctcttgttgttctggcttcatgg
   49 ----------------------------------------------------
      tctttactctggcagataagtcaaggaccccgagaacaacaagaccgaagtacc

         [M  R  P  S  I  Q  F  L  G  L  L  L  F  W  L  H  G
                                  LEADER

      tgctcagtgtgacatccagatgacacagtctccatcctcactgtctgcatctct
  103 ----------------------------------------------------
      acgagtcacactgtaggtctactgtgtcagaggtaggagtgacagacgtagaga

       A  Q  C][D  I  Q  M  T  Q  S  P  S  S  L  S  A  S  L
                                                  FR1
      gggaggcaaagtcaccatcacttgcaagacaagccaagacattaacaagtatat
  157 ----------------------------------------------------
      ccctccgtttcagtggtagtgaacgttctgttcggttctgtaattgttcatata

       G  G  K  V  T  I  T  C][K  T  S  Q  D  I  N  K  Y  M
                                     CDR1

      ggcttggtaccaacacaagcctggaaaacgtcctaggctgctcatacattacac
  211 ----------------------------------------------------
      ccgaaccatggttgtgttcggacctttgcaggatccgacgagtatgtaatgtg

       A][W  Y  Q  H  K  P  G  K  R  P  R  L  L  I  H][Y  T
                                FR2

      atctgcattacagccaggcatcccatcaaggttcagtggaagtgggtctgggag
  265 ----------------------------------------------------
      tagacgtaatgtcggtccgtagggtagttccaagtcaccttcacccagaccctc

       S  A  L  Q  P][G  I  P  S  R  F  S  G  S  G  S  G  R
       CDR2
```

FIG. 11 A

```
    agattattccttcaacatcagcaacctggagcctgaagatattgcaacttatta
319 ----------------------------------------------------
    tctaataaggaagttgtagtcgttggacctcggacttctataacgttgaataat

     D  Y  S  F  N  I  S  N  L  E  P  E  D  I  A  T  Y  Y
           FR3

    ttgtctacagtatgataatctgtggacgttcggtggaggcaccaagctggaaat
373 ----------------------------------------------------
    aacagatgtcatactattagacacctgcaagccacctccgtggttcgaccttta

     C][L  Q  Y  D  N  L  W  T][F  G  G  G  T  K  L  E  I
           CDR3                          FR4


    caaacgggctgatgctgcaccaactgtatccatcttcccaccatccacccggga
427 ----------------------------------------------------
    gtttgcccgactacgacgtggttgacataggtagaagggtggtaggtgggccct

     K]

    AGG-5'
    tcc
481 ---
    agg
```

FIG. 11B

```
          atgaaatgcagctgggtcatgttcttcctgatggcagtggttacaggg
        1 ----------------------------------------------
          tactttacgtcgacccagtacaagaaggactaccgtcaccaatgtccc

             [M  K  C  S  W  V  M  F  F  L  M  A  V  V  T  G
                                  LEADER

          gtcaattcagaggttcagctgcagcagtctggggcagagcttgtgaagccaggg
       49 ----------------------------------------------------
          cagttaagtctccaagtcgacgtcgtcagaccccgtctcgaacacttcggtccc

          V  N  S][E  V  Q  L  Q  Q  S  G  A  E  L  V  K  P  G
                                                  FR1

          gcctcagtcaagttgtcctgcacagcttctggcttcaacattaaagacacctat
      103 ----------------------------------------------------
          cggagtcagttcaacaggacgtgtcgaagaccgaagttgtaatttctgtggata

          A  S  V  K  L  S  C  T  A  S  G  F  N  I  K][D  T  Y
                                                       CDR1

          atacactgtgtgaagcagaggcctgaacagggcctggagtggattggaaggatt
      157 ----------------------------------------------------
          tatgtgacacacttcgtctccggacttgtcccggacctcacctaaccttcctaa

          I  H][C  V  K  Q  R  P  E  Q  G  L  E  W  I  G][R  I
                                  FR2

          gatcctgcgaatggttatactaaatatgacccgaagttccagggcaaggccact
      211 ----------------------------------------------------
          ctaggacgcttaccaatatgatttatactgggcttcaaggtcccgttccggtga

          D  P  A  N  G  Y  T  K  Y  D  P  K  F  Q  G][K  A  T
                         CDR2

          ataacagctgacacatcctccaacacagcctacctgcagctcagcagcctgaca
      265 ----------------------------------------------------
          tattgtcgactgtgtaggaggttgtgtcggatggacgtcgagtcgtcggactgt

          I  T  A  D  T  S  S  N  T  A  Y  L  Q  L  S  S  L  T
                                                  FR3
```

FIG. 12A

```
    tctgaggacactgccgtctatttctgtgctagagagggatattatggtaactac
319 ----------------------------------------------------
    agactcctgtgacggcagataaagacacgatctctccctataataccattgatg

    S  E  D  T  A  V  Y  F  C  A  R][E  G  Y  Y  G  N  Y
                                                 CDR3

    ggggtctatgctatggactactggggtcaaggaacctcagtcaccgtctcctca
373 ----------------------------------------------------
    ccccagatacgatacctgatgaccccagttccttggagtcagtggcagaggagt

    G  V  Y  A  M  D  Y][W  G  Q  C  T  S  V  T  V  S  S]


    gccaaaacgacaccccatctgtctatccactggcccgggatcc
427 ----------------------------------------
    cggttttgctgtgggggtagacagataggtgaccgggccctagg

    S  S]
```

FIG. 12B

```
                FR1                      CDR1         FR2            CDR2
             1               2             3            4              5
     12345678901234567890123  45678901234  567890123456789  0123456
      *                       *********                 *    ***
21.6 DIQMTQSPSSLSASLGGKVTITC  KTSQDINKYMA  WYQHKPGKRPRLLIH  YTSALQP

REI  DIQMTQSPSSLSASVGDRVTITC  QASQDIIKYLN  WYQQTPGKAPKLLIY  EASNLQA

La   DIQMTQSPSSLSASVGDRVTITC  KTSQDINKYMA  WYQQTPGKAPRLLIH  YTSALQP

Lb   -----------------------  -----------  ----------R----  -------


                       FR3                          CDR3       FR4
      6          7          8           9          10
     78901234567890123456789012345678  901234567  8901234567
              *        *               *******
21.6 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYC  LQYDNL-WT  FGGGTKLEIK

REI  GVPSRFSGSGSGTDYTFTISSLQPEDIATYYC  QQYQSLPYT  FGQGTKLQIT

La   GIPSRFSGSGSGRDYTFTISSLQPEDIATYYC  LQYDNL-WT  FGQGTKVEIK

Lb   -I----------R-------------------  ---------  ------VE-K
```

FIG. 13

```
                    FR1              CDR1       FR2           CDR2
               1         2         3           4          5          6
      123456789012345678901234567890 12345 67890123456789 012A3456789012345
                               ***** ** *                    ****
21.6  EVQLQQSGAELVKPGASVKLSCTASGFNIK DTYIH CVKQRPEQGLEWIG RIDPANGYTKYDPKFQG

2*CL  QVQLVQSGAEVKKPGASVKVSCKASGYTFT SYAMH WVRQAPGQRLEWMG WINAGNGNTKYSQKFQG

Ha    QVQLVQSGAEVKKPGASVKVSCKASGFNIK DTYIH WVRQAPGQRLEWMB RIDPANGYTKYDPKFQG

Hb    --------------------------FNIK ----- --------G----- -----------------

Hc    --------------------------FNIK ----- -------------- -----------------
```

```
                      FR3                  CDR3         FR4
          7         8            9         10               11
      67890123456789012ABC345678901234 567890ABCDEF12 34567890123
           *                         *
21.6  KATITADTSSNTAYLQLSSLTSEDTAVYFCAR EGYYGNYGVYAMDY WGQGTSVTVSS

2*CL  RVTITRDTSASTAYMELSSLRSEDTAVYYCAR GGYYGSGS----NY WGQGTLVTVSS

Ha    RVTITADTSASTAYMELSSLRSEDTAVYYCAR EGYYGNYGVYAMDY WGQGTLVTVSS

Hb    -----A-------------------------- -------------- -----------

Hc    -----A-------------------------- ---F---------- -----------
```

FIG. 14

HindIII KOZAK SEQUENCE

```
    aagcttgccgccaccatgagaccgtctattcagttcctggggctcttgttgttc
1   ----------------------------------------------------
    ttcgaacggcggtggtactctggcagataagtcaaggaccccgagaacaacaag

                  [M  R  P  S  I  Q  F  L  G  L  L  L  F
                                          LEADER

    tggcttcatggtgctcagtgtgacatccagatgacacagtctccatcctcactg
55  ----------------------------------------------------
    accgaagtaccacgagtcacactgtaggtctactgtgtcagaggtaggagtgac

    W  L  H  G  A  Q  C][D  I  Q  M  T  Q  S  P  S  S  L
                                                    FR1

    tctgcatctGTAggaGATAGAgtcaccatcacttgcaagacaagccaagacatt
109 ----------------------------------------------------
    agacgtagaCATcctCTATCTcagtggtagtgaacgttctgttcggttctgtaa

    S  A  S  V  G  D  R  V  T  I  T  C][K  T  S  Q  D  I
                                             CDR1

    aacaagtatatggcttggtaccaaCAGACAcctggaaaaGCTcctaggctgctc
163 ----------------------------------------------------
    ttgttcatataccgaaccatggttGTCTGTggacctttttCGAggatccgacgag

    N  K  Y  M  A][W  Y  Q  Q  T  P  G  K  A  P  R  L  L
                                 FR2

    atacattacacatctgcattacagccaggcatcccatcaaggttcagtggaagt
217 ----------------------------------------------------
    tatgtaatgtgtagacgtaatgtcggtccgtagggtagttccaagtcaccttca

    I  H][Y  T  S  A  L  Q  P][G  I  P  S  R  F  S  G  S
             CDR2

    gggtctgggagagattatACTttcACCatcagcAGCctgCAGcctgaagatatt
271 ----------------------------------------------------
    cccagaccctctctaataTGAaagTGGtagtcgTCGgacGTCggacttctataa

    G  S  F  R  D  Y  T  F  T  I  S  S  L  Q  P  E  D  I
                FR3
```

FIG. 15A

```
    gcaacttattattgtctacagtatgataatctgtggacgttcggtCAAggcacc
325 ----------------------------------------------------------
    cgttgaataataacagatgtcatactattagacacctgcaagccaGTTccgtgg

    A  T  Y  Y  C][L  Q  Y  D  N  L  W  T][F  G  Q  G  T
                              CDR3                    FR4

         SPLICE DONOR SITE BamHI
    aagGTGgaaatcaaacgtgagtggatcc
379 --------------------------
    ttcCACctttagtttgcactcacctagg

    K  V  E  I  K]
```

FIG. 15B

```
   HindIII KOZAK SEQUENCE
    AAGCTTGCCGCCACCATGGACTGGACCTGGCGCGTGTTTTGCCTGCTCGCCGTG
  1 ----------------------------------------------------
    TTCGAACGGCGGTGGTACCTGACCTGGACCGCGCACAAAACGGACGAGCGGCAC

                    [M  D  W  T  W  R  V  F  C  L  L  A  V
                                                LEADER

    GCTCCTGGGGCCCACAGCCAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAG
 55 ----------------------------------------------------
    CGAGGACCCCGGGTGTCGGTCCACGTTGATCACGTCAGGCCGCGGCTTCACTTC

    A  P  G  A  H  S][Q  V  Q  L  V  Q  S  G  A  E  V  K

    AAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAGCTAGCGGTttcaacattaaa
109 ----------------------------------------------------
    TTTGGGCCACGAAGGCACTTTCAGTCGACATTTCGATCGCCAaagttgtaattt

    K  P  G  A  S  V  K  V  S  C  K  A  S  G  F  N  I  K][
          FR1

    gacacctatatacactGGGTTAGACAGGCCCCtGGCCAAaGGCTgGAGTGGATg
163 ----------------------------------------------------
    ctgtggatatatgtgACCCAATCTGTCCGGgGaCCGGTTtCCGAcCTCACCTAc

    D  T  Y  I  H][W  V  R  Q  A  P  G  Q  R  L  E  W  M
       CDR1                          FR2
```

FIG. 16A

```
    GGaaggattgatcctgcgaatggttatactaaatatgacccgaagttccagggc
217 ----------------------------------------------------------
    CCttcctaactaggacgcttaccaatatgatttatactgggcttcaaggtcccg

    G][R  I  D  P  A  N  G  Y  T  K  Y  D  P  K  F  Q  G][
                                  CDR2

    cgggtcACCatcACCgcaGACACCTCTgccagcACCGCCTACATGGAACTGTCC
271 ----------------------------------------------------------
    gcccagTGGtagTGGcgtCTGTGGAGAcggtcgTGGCGGATGTACCTTGACAGG

    R  V  T  I  T  A  D  T  S  A  S  T  A  Y  M  E  L  S
                                                        FR3

    AGCCTGCGCTCCGAGGACACTGCAGTCTACTACTGCGCCagagagggatattat
325 ----------------------------------------------------------
    TCGGACGCGAGGCTCCTGTGACGTCAGATGATGACGCGGtctctccctataata

    S  L  R  S  E  D  T  A  V  Y  Y  C  A  R][E  G  Y  Y

    ggtaactacggggtctatgctatgGACTAcTGGGGtCAaGGaACCCTTGTCACC
379 ----------------------------------------------------------
    ccattgatgccccagatacgatacCTGATgACCCCaGTtCCtTGGGAACAGTGG

    G  N  Y  G  V  Y  A  M  D  Y][W  G  Q  G  T  L  V  T
          CDR3                                        FR4

    SPLICE DONOR SITE BamHI
    GTCtccTCAGGTGAGTGGATCC
433 ----------------------
    CAGaggAGTCCACTCACCTAGG

    V  S  S]
```

FIG. 16B

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys - C

FIG. 17A

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ser Leu Val Xaa
Xaa Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
Tyr Asn Ser Leu Pro Glu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
Ile Lys - C

FIG. 17B

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

N - Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe
Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
Ala Arg Gly Tyr Tyr Tyr Tyr Asp Ser Xaa Val Gly Tyr Tyr Ala Met
Asp Tyr Trp Gly Gln Gly Thr Xaa Val Thr Val Ser Ser - C

FIG. 18A

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

N - Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
Gly Trp Ile Asn Pro Tyr Gly Asn Gly Asp Thr Asn Tyr Ala Gln Lys
Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
Cys Ala Arg Ala Pro Gly Tyr Gly Ser Gly Gly Gly Cys Tyr Arg Gly Asp
Tyr Xaa Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser - C

FIG. 18B

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☑ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.
As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.